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Fig. 1

Aldotetrose 4	DEry	D-Erythrose
	DThr	D-Threose
	LEry	L-Erythrose
	LThr	L-Threose
Ketotetrose 2	DEry	D-Erythrulose
	LEry	L-Erythrulose
Tetritol 3	D,LEry	D-,L-Erythritol
	DThr	D-Threitol
(Tetroses 9)	LThr	L-Threitol
Aldopentose 8	DRib	D-Ribose
	DAra	D-Arabinose
	DXyl	D-Xylose
	DLyx	D-Lyxose
	LRib	L-Ribose
	LAra	L-Arabinose
	LXyl	L-Xylose
	LLyx	L-Lyxose
Ketopentose 4	DRib	D-Ribulose
	DXyl	D-Xylulose
	LRib	L-Ribulose
	LXy	L-Xylulose
Pentitol 4	D,LRib	D-Ribitol,L-Ribitol
	DAra	D-Arabitol
	D,LXyl	D-Xylitol,L-Xylitol
(Pentoses 16)	LAra	L-Arabitol
Aldohexose 16	DAll	D-Allose
	DAlt	D-Altrose
	DGlu	D-Glucose
	DMan	D-Mannose
	DGul	D-Gulose
	DIdo	D-Idose
	DGal	D-Galactose
	DTal	D-Talose
	LAll	L-Allose
	LAlt	L-Altrose
	Lglu	L-Glucose
	DMan	L-Mannose
	LGul	L-Gulose
	LIdo	L-Idose
	LGal	L-Galactose
	LTal	L-Talose
Ketohexose 8	DFru	D-Fructose
	DPsi	D-Psicose
	DSor	D-Sorbose
	DTag	D-Tagatose
	LFru	L-Fructose
	LPsi	L-Psicose
	LSor	L-Sorbose
	LTag	L-Tagatose
Hexitol 10	D,LAll	D-Allitol,L-Allitol
	DAlt,DTal	D-Altritol,D-Talitol
	DGlu,LGul	D-Glucitol,L-Gulitol
	DMan	D-Mannitol
	DGul,LGlu	D-Gulitol,L-Glucitol
	DIdi	D-Iditol
	D,LGal	D-Galactitol,L-Galactitol
	LAlt,LTal	L-Altritol,L-Talitol
	LMan	L-Mannitol
(Hexoses 34)	LIdi	L-Iditol

Biosynthesis strategy for all monosaccharides using **Izumoring**

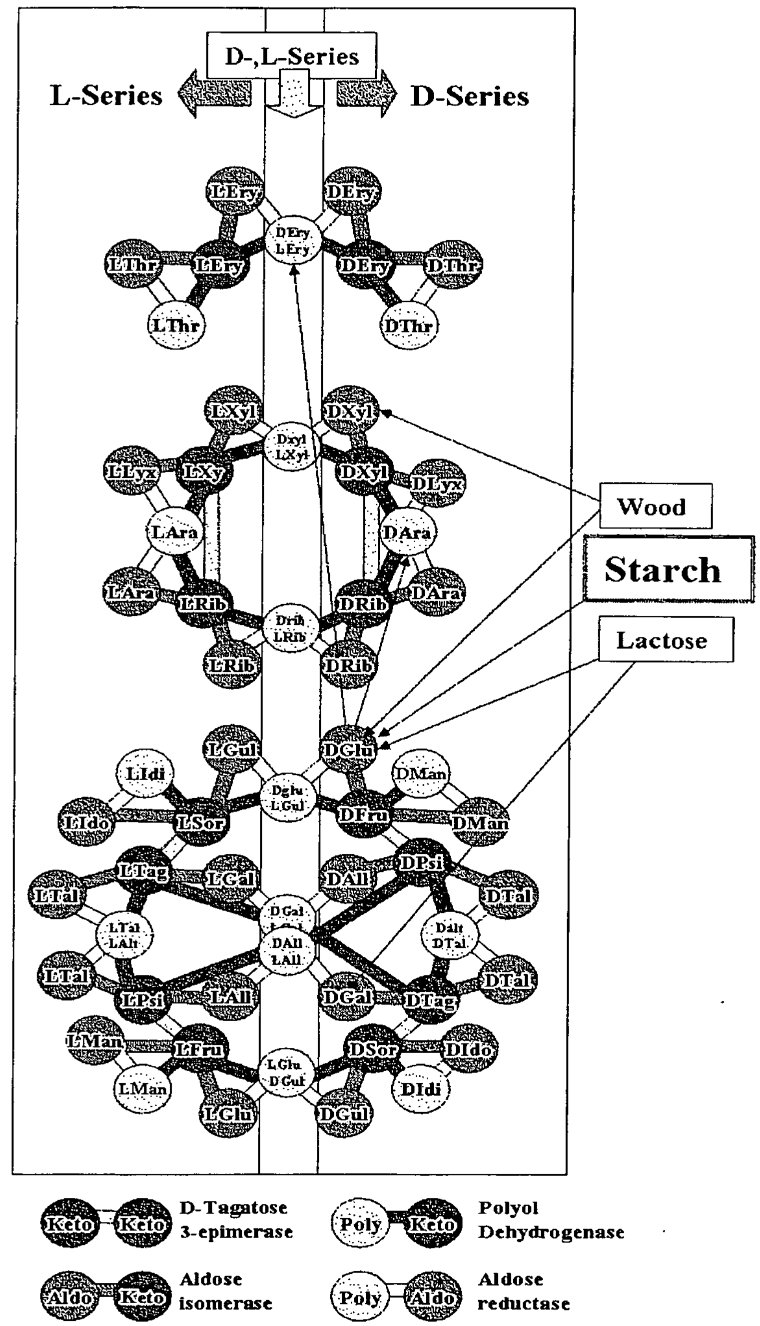

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Fig. 2

```
1    ATGGCTGAATTCAGGATCGCTCAGGATGTCGTTGCGCGGGAAAACGACAGGCGCGCCTCG   60
1    M  A  E  F  R  I  A  Q  D  V  V  A  R  E  N  D  R  R  A  S    20
61   GCGCTGAAGGAAGACTACGAGGCGCTCGGCGCGAATCTCGCCCGCCGTGGCGTCGACATC  120
21   A  L  K  E  D  Y  E  A  L  G  A  N  L  A  R  R  G  V  D  I    40
121  GAGGCCGTCACGGCCAAGGTCGAAAAGTTCTTCGTCGCCGTCCCCTCCTGGGGCGTCGGC  180
41   E  A  V  T  A  K  V  E  K  F  F  V  A  V  P  S  W  G  V  G    60
181  ACGGGCGGCACGCGCTTTGCGCGCTTCCCCGGCACCGGCGAGCCGCGCGGCATCTTCGAC  240
61   T  G  G  T  R  F  A  R  F  P  G  T  G  E  P  R  G  I  F  D    80
241  AAGCTGGACGACTGCGCCGTCATCCAGCAGCTGACACGCGCCACGCCCAATGTCTCGCTG  300
81   K  L  D  D  C  A  V  I  Q  Q  L  T  R  A  T  P  N  V  S  L   100
301  CATATTCCGTGGGACAAGGCCGATCCGAAGGAGCTGAAGGCCAGGGGCGACGCCCTCGGC  360
101  H  I  P  W  D  K  A  D  P  K  E  L  K  A  R  G  D  A  L  G   120
361  CTCGGCTTCGACGCGATGAACTCCAATACCTTCTCCGATGCGCCCGGCCAGGCGCATTCC  420
121  L  G  F  D  A  M  N  S  N  T  F  S  D  A  P  G  Q  A  H  S   140
421  TACAAATACGGCTCGCTCAGCCACACGGATGCGGCAACGCGCGCCCAGGCGGTCGAGCAC  480
141  Y  K  Y  G  S  L  S  H  T  D  A  A  T  R  A  Q  A  V  E  H   160
481  AATCTGGAATGCATCGAGATCGGCAAGGCCATCGGCTCCAAGGCGCTGACGGTCTGGATC  540
161  N  L  E  C  I  E  I  G  K  A  I  G  S  K  A  L  T  V  W  I   180
541  GGTGACGGCTCCAACTTCCCCGGCCAGAGTAACTTCACCAGGGCTTTCGAACGTTATCTC  600
181  G  D  G  S  N  F  P  G  Q  S  N  F  T  R  A  F  E  R  Y  L   200
601  TCGGCGATGGCGGAGATCTACAAGGGCCTGCCGGATGACTGGAAGCTGTTCTCCGAGCAC  660
201  S  A  M  A  E  I  Y  K  G  L  P  D  D  W  K  L  F  S  E  H   220
661  AAGATGTACGAGCCGGCCTTCTATTCGACCGTCGTGCAGGACTGGGGCACGAATTATCTC  720
221  K  M  Y  E  P  A  F  Y  S  T  V  V  Q  D  W  G  T  N  Y  L   240
721  ATCGCCCAGACGCTCGGCCCCAAGGCCCAGTGCCTCGTCGATCTCGGCCATCACGCGCCG  780
241  I  A  Q  T  L  G  P  K  A  Q  C  L  V  D  L  G  H  H  A  P   260
781  AACACCAATATCGAGATGATCGTCGCCCGGCTCATCCAGTTCGGCAAGCTCGGCGGCTTC  840
261  N  T  N  I  E  M  I  V  A  R  L  I  Q  F  G  K  L  G  G  F   280
841  CATTTCAACGATTCCAAATACGGCGACGACGACCTCGATGCCGGCGCCATCGAGCCCTAT  900
281  H  F  N  D  S  K  Y  G  D  D  D  L  D  A  G  A  I  E  P  Y   300
901  CGCCTCTTCCTCGTCTTCAACGAGCTGGTGGATGCGGAGGCGCGCGGCGTCAAGGGCTTC  960
301  R  L  F  L  V  F  N  E  L  V  D  A  E  A  R  G  V  K  G  F   320
961  CACCCGGCCCACATGATCGACCAGTCGCACAACGTCACCGACCCGATCGAGAGCCTGATC 1020
321  H  P  A  H  M  I  D  Q  S  H  N  V  T  D  P  I  E  S  L  I   340
1021 AACAGCGCGAACGAAATCCGTCGCGCCTATGCGCAGGCCCTCCTTGTCGACCGCGCGGCG 1080
341  N  S  A  N  E  I  R  R  A  Y  A  Q  A  L  L  V  D  R  A  A   360
1081 CTTTCCGGCTACCAGGAGGACAACGACGCCCTGATGGCGACGGAAACGTTGAAGCGCGCC 1140
361  L  S  G  Y  Q  E  D  N  D  A  L  M  A  T  E  T  L  K  R  A   380
1141 TACCGTACCGATGTGGAGCCGATCCTCGCCGAGGCCCGCCGCCGCACGGGCGGCGCCGTC 1200
381  Y  R  T  D  V  E  P  I  L  A  E  A  R  R  R  T  G  G  A  V   400
1201 GACCCCGTCGCGACCTATCGGGCCAGCGGCTACCGCGCCAGGGTCGCCGCCGAGCGCCCC 1260
401  D  P  V  A  T  Y  R  A  S  G  Y  R  A  R  V  A  A  E  R  P   420
1261 GCCTCCGTCGCGGGTGGCGGCGGCATCATCTGA 1293
421  A  S  V  A  G  G  G  G  I  I  *   431
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Fig. 3

```
M---AEFRIAQDVVARENDRRASALKEDYEALGANLARRGVDIEAVTAKVEKFFVA--VP  55
MTIKANYDSAKQAYEKWGIDVEEALRQLEQVPISIHCWQGDDIEGFEVNKGELSGGIDVT  60

SWGVGTGGTRFARFPGTGEPRGIFDKLDDCAVIQQLTRATPNVSLHIPWDKADPKELKAR  115
GNYPGKAQTPEELRRDLEKALSLIPGKHRVNLHAIYAETNREAVERDELKPQHFENWVKW  120

GDALGLGFDAMNSNTFSDAPGQAHSYKYGSLSHTDAATRAQAVEHNLECIEIGKAIGSKA  175
AKNLGLGLDFNPTLFSHEKAADGLT-----LSHPDPDIREFWIRHCIACRRIGEYFGKEL  175

LTVWIGDGSNFPGQSNFTR----AFERYLSAMAEIY-KGLPDDWKLFS-EHKMYEPAFYS  229
GTPCLTNIWIPDGYKDIPSDRLTPRKRLKESLDRIFSEEISEQHNLDSIESKLFGLGSES  235

TVVQDWGTNYLIAQTLGPKAQCLVDLGH-HAPNTNIEMIVARLIQFGKLGGFHFNDSKYG  288
YVV--GSHEFYLAYALTNHKLCLLDTGHFHPTETVSNKISSMLLYTDKLA-LHVSRPVRW  292

DDDLDAGAIEPYRLFLVFNELVDAEARGVKGFHPAHMIDQSHNVTDPIESLINSANEIRR  348
DSDHVVVLDDELR------EIALEIVRNHALEKVAIGLDFFDASINRVAAWTIGTRNMIK  346

AYAQALLVDRAALSGYQEDNDALMATETLKRAYRTDVEPILAEARRRTGGAVDPVATYRA  408
ALLYALLLPNGYLKQLQEEGRYTERLALMEEFKTYPFGAIWDSYCEQMGVPVKEAWLYDI  406

SGYRARVAAERPASVAGGGGII  430
KEYEQQVLLKRKASSP----IV  424
```

上: *Pseudomonas stutzerii*
下: *Bacillus subtilis*

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Fig. 4

```
RhI    MAEFRIAQDVVARENDRRASALKEDYEALGANLARRGVDIEAVTAKVEKFFVAVPSWGVG   60
SISTR  MTE------------------------------------LAAVKAALKTQAVETPSWAYG   24
SITHE  MI------------------------------------NMERIFKELDELKFELPSWAFS   24

RhI    TGGTRFARFPGTGEPRGIFDKLDDCAVIQQLTRATPNVSLHIPWDKA-DPKELKARGDAL  119
SISTR  NSGTRFKVFAQPGVPRDPFEKLDDAAKVHEFTGAAPTVALHIPWDRVEDYAALAAHAEKR   84
SITHE  DAGTRFAVFHEEGAARNVFERIEDAALVHRLTGCCPSVALHIPWDKVENWEELREFAEEK   84

RhI    GLGFDAMNSNTFSDAPGQAHSYKYGSLSHTDAATRAQAVEHNLECIEIGKAIGSKALTVW  179
SISTR  GVRIGAINSNTFQDD-----DYRLGSICHPDAAVRRKAVDHLLECVDIMDATGSRDLKLW  139
SITHE  GLKIGAINPNLFQDP-----DYKYGSLTNPSEKIRKKAIAHVMECVDIAEKTGSKVISLW  139

RhI    IGDGSNFPGQSNFTRAFERYLSAMAEIYKGLPDDWKLFSEHKMYEPAFYSTVVQDWGTNY  239
SISTR  FADGTNYPGQDDIRSRQDRLAEGLAEVYERLGEGQRMLLEYKLFEPAFYTTDVPDWGTAY  199
SITHE  LADGTDYPGQDDFRSRKKRLEESLRYIYENMPADMYLLIEYKFFEPAFYHTDIPDWGMSY  199

RhI    LIAQTLGPKAQCLVDLGHHAPNTNIEMIVARLIQFGKLGGFHFNDSKYGDDDLDAGAIEP  299
SISTR  AHCLKLGEKAQVVVDTGHHAPGTNIEFIVATLLREGKLGGFDFNSRFYADDDLMVGAADP  259
SITHE  LLSEKLGERALVLVDLGHHPQGTNIEYIVATLLSEKKLGGFHLNNRKYADDDLTIASINP  259

RhI    YRLFLVFNELVDAEARGVKGFH---PAHMIDQSHNVTDPIESLINSANEIRRAYAQALLV  356
SISTR  FQLFRI---MYEVVRGGGFTSD---VAFMLDQCHNIEAKIPAIIRSVMNVQEATAKALLV  313
SITHE  YEVFLIFKEIVFAKRDPELSDSAKKVVLMFDQAHITKPKILAMIQSVLIAQELFTKALLI  319

RhI    DRAALSGYQEDNDALMATETLKRAYRTDVEPILAEARRRTGGAVDPVATYRASGYRARVA  416
SISTR  DGTALAEAQAAGDVLEANAVLMDAYNTDVRPLLREVREESGLDPEPMKAYRSCGWAEKVV  373
SITHE  DENRLREAQKNYDVVEAEEILLDAFRTDVRPILREYRRQKGLPEDPLRVFREEDYMEKRR  379

RhI    AERPASVAGGGGII  430
SISTR  AERIGGQQAGWG-A  386
SITHE  RERR----------  383
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Fig. 5

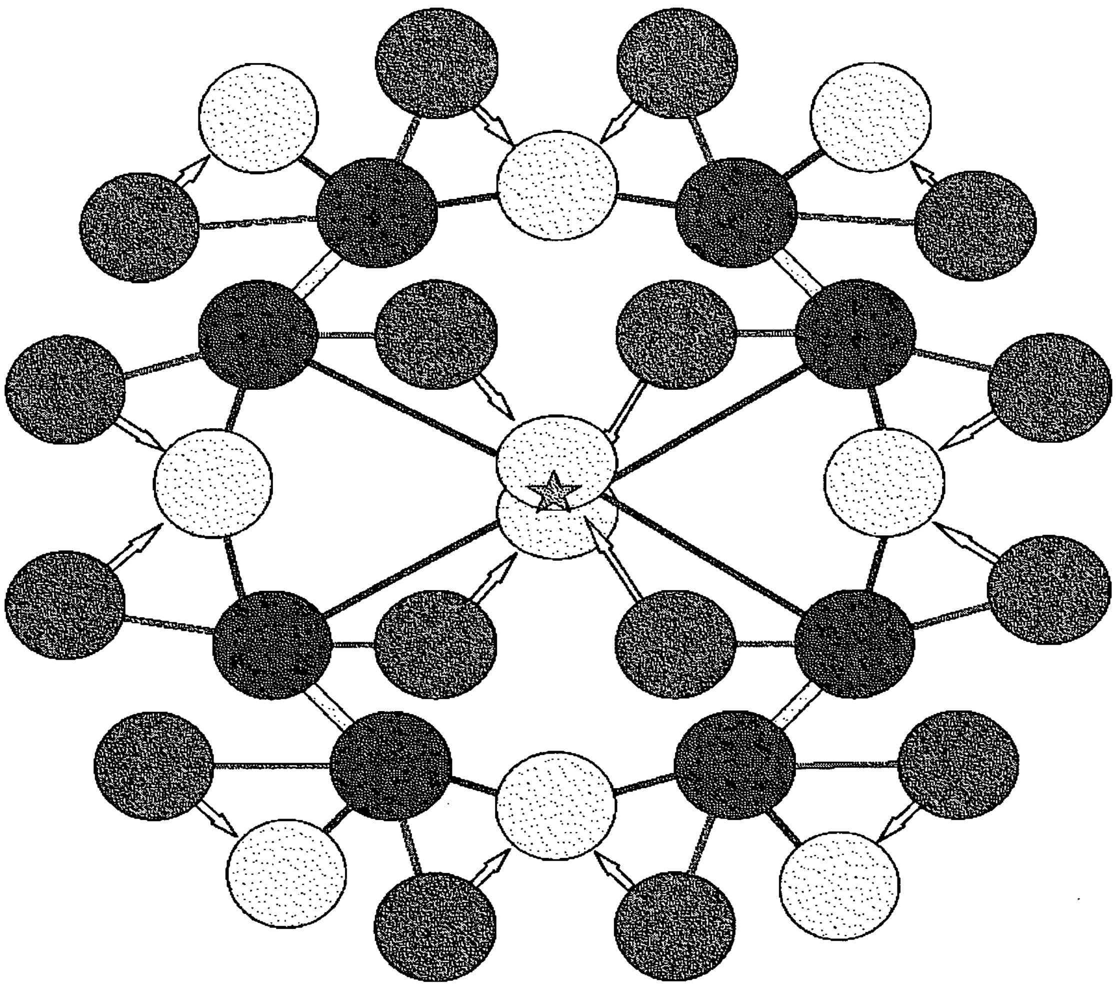

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Fig. 6

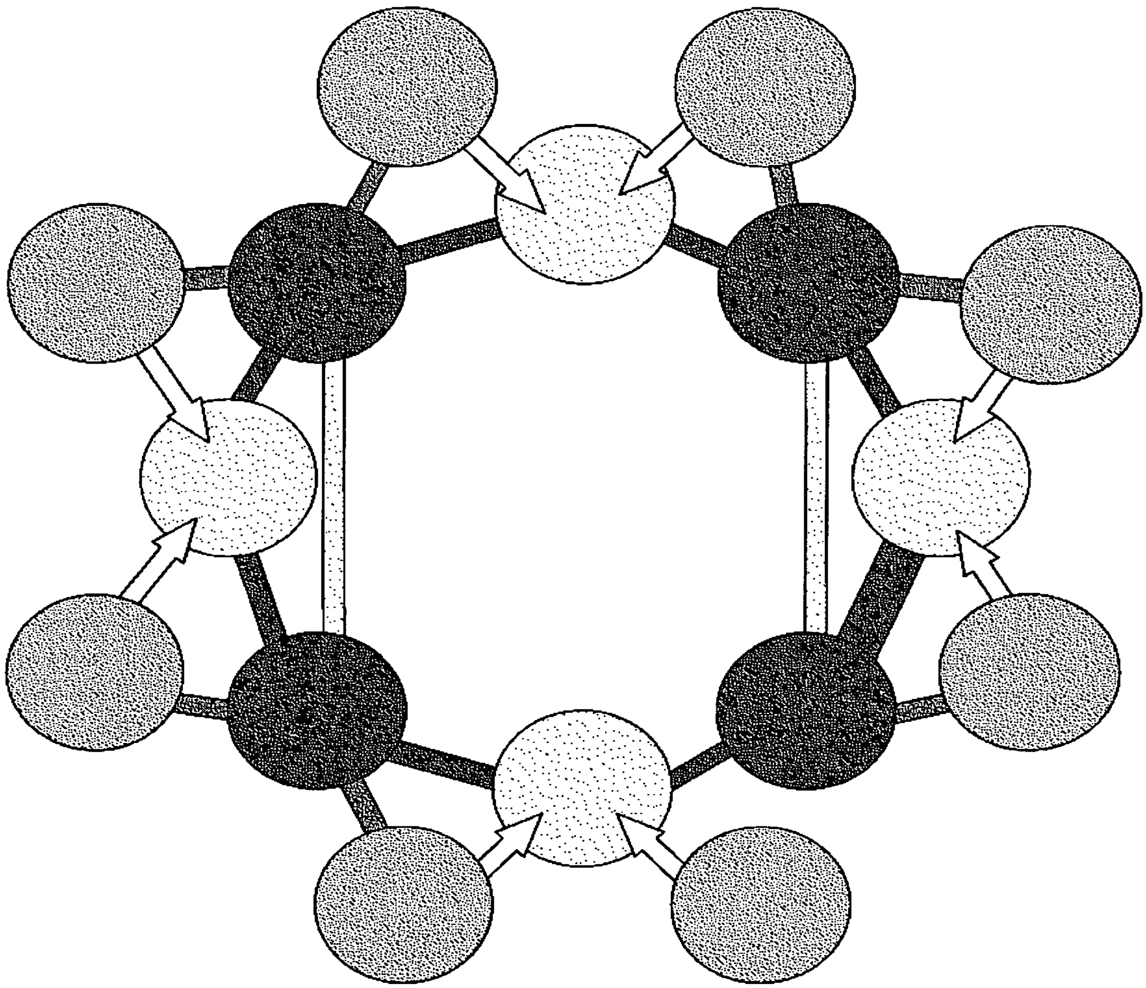

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Fig. 7

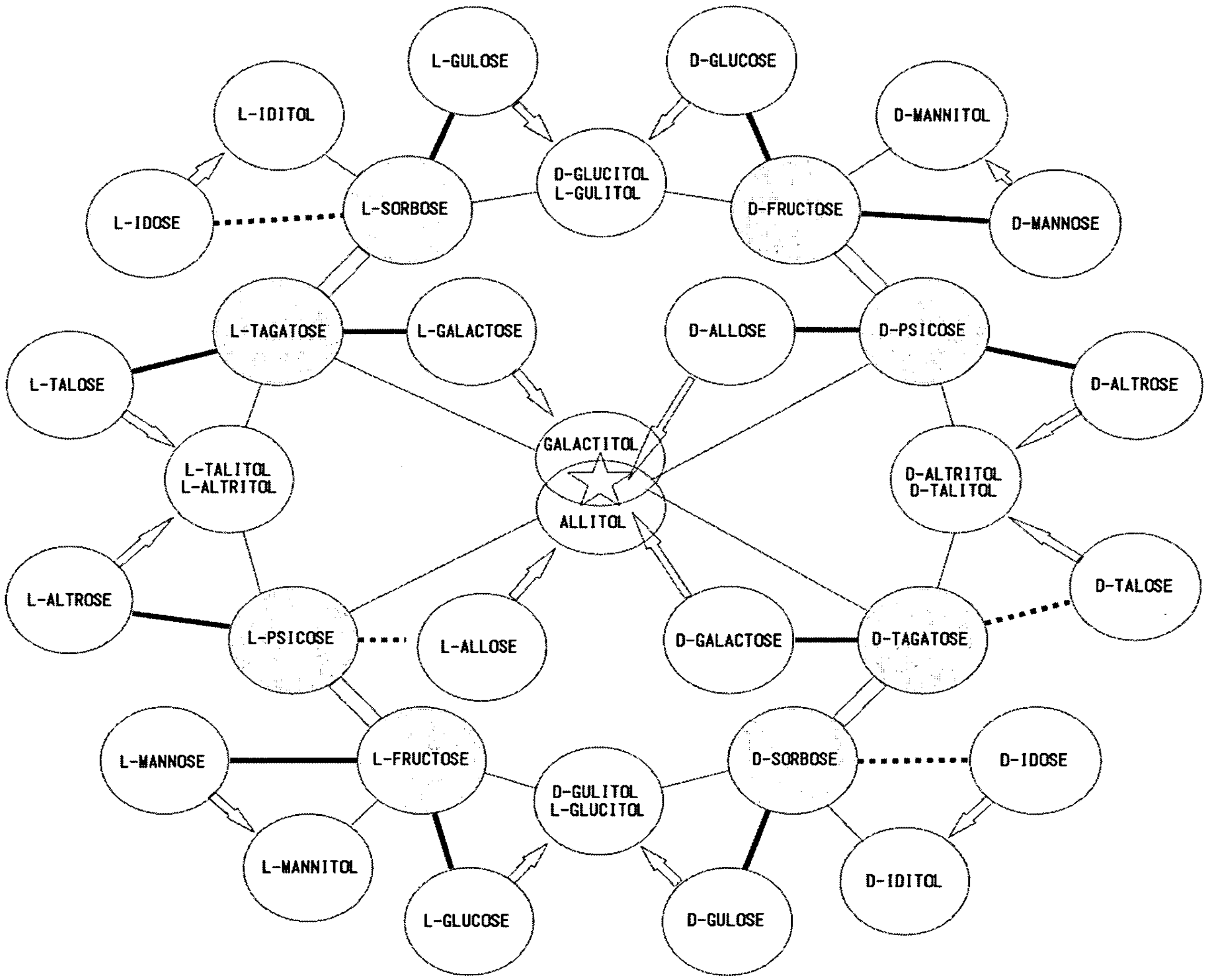

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Fig. 8

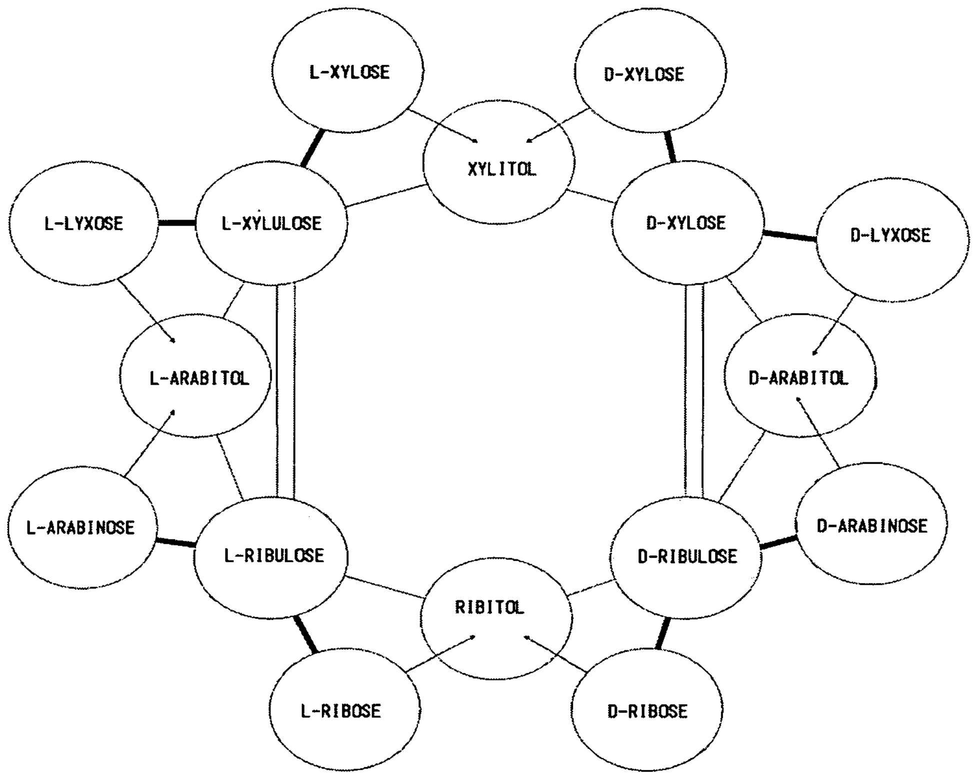

Fig. 9

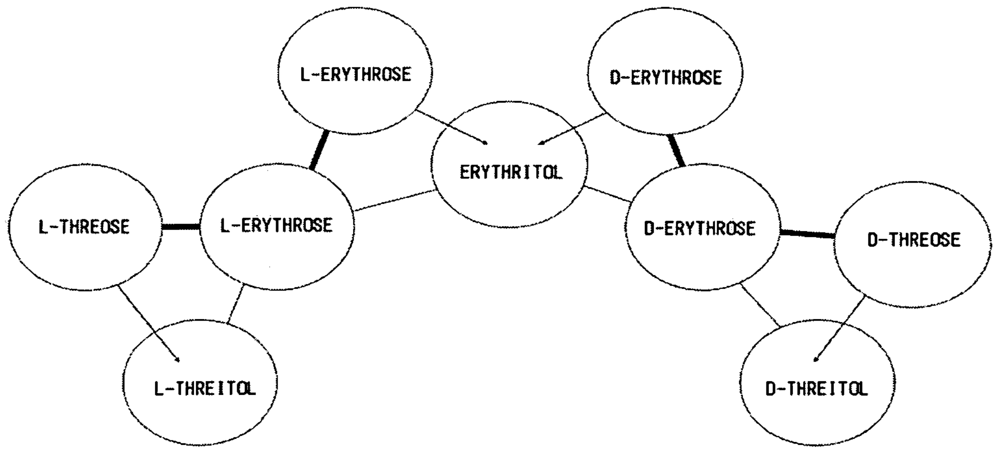
L-ERYTHROSE
D-ERYTHROSE
ERYTHRITOL
L-THREOSE
L-ERYTHROSE
D-ERYTHROSE
D-THREOSE
L-THREITOL
D-THREITOL

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Fig. 10